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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/285,306	04/02/99	GINGERAS	T 018547-018557

020350
TOWNSEND AND TOWNSEND AND CREW
TWO EMBARCADERO CENTER
EIGHTH FLOOR
SAN FRANCISCO CA 94111-3834

HM22/0129

EXAMINER	
SIEW, J	
ART UNIT	**PAPER NUMBER**
1656	17

DATE MAILED: 01/29/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

Office Action Summary	Application No. 09/285,306	Applicant(s) GINGERAS ET AL.	
	Examiner Jeffrey Siew	Art Unit 1656	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 1 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136 (a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *11,12, 13 November 2000* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-20* is/are pending in the application.

4a) Of the above claim(s) *17-20* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☐ Claim(s) *1-16* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☒ Claims *1-20* are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *02 April 1999* is/are objected to by the Examiner.

11)☒ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. § 119

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. & 119(e).

Attachment(s)

15) ☒ Notice of References Cited (PTO-892)
16) ☒ Notice of Draftsperson's Patent Drawing Review (PTO-948)
17) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
18) ☒ Interview Summary (PTO-413) Paper No(s). 15.
19) ☐ Notice of Informal Patent Application (PTO-152)
20) ☒ Other: *STIC Sequence match* .

DETAILED ACTION

Election/Restrictions

1. Applicant's election without traverse of Group I in Paper No. 11 is acknowledged.

Claims 17-20 withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected Group II, there being no allowable generic or linking claim. Election was made **without** traverse in Paper No.13.

Drawings

2. New formal drawings are required in this application because Figure 1 is confusing. The sequences require proper sequence identifier numbers and it is suggested that corrections such as further labeling of Figure and base pair numbering would help to clarify the Figure. Applicant is advised to employ the services of a competent patent draftsperson outside the Office, as the Patent and Trademark Office no longer prepares new drawings. Applicant is referred to MPEP 608.02(p) to effect Drawing amendments.

Specification

3. It is noted that the amendment filed 7/23/99 & 7/24/00 to the drawings have not been entered. It is advised that a proper amendment with the proposed Table to be incorporated be submitted. Future amendments will be considered accordingly (in addition see also paragraph 2).

4. In the Brief Description of Drawings the description of Figure 3 & 4 is missing.

5. The status to related applications should be updated e.g. page 1, line 15.

Claim Rejections - 35 USC § 101

6. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1 & 2 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

Claims 1 & 2 read on a DNA coding sequence per se which is found in nature and thus, is unpatentable to applicant. The DNA molecule, as claimed, has the same characteristics and utility as those found naturally in the genome or as cellular precursors thereof and therefore does

not constitute patentable subject matter. See American Wood v. Fiber Disintegrating Co., 90 U.S. 566 (1974), American Fruit Growers v. Brodgex Co., 283 U.S. 2 (1931), Funk Brothers Seed Co. v. Kalo Inoculant Co., 33 U.S. 127 (1948), Diamond v. Chakrabarty, 206 USPQ 193 (1980). It is suggested that applicant use the language "isolated" (see specification page 4 line 15) in connection with the DNA coding sequence to identify a product that is not found in nature.

Claim Rejections - 35 USC § 112

7. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

8. Claims 1-16 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A) Claims 1-14 are indefinite because it cannot be determined as to whether the nucleic acid encompasses any one of the listed sequences, any part of the listed sequences or any combination of the sequences or a sequence comprising any one of the listed sequences. The metes and bounds of the claims cannot be determined. It is recommended that proper Markush language be incorporated.

B) The term "complete" renders claims 2 indefinite. It cannot be determined as what criteria would define the completeness of the sequence e.g. an open reading frame (ORF) or the listed sequence etc. Similarly, the term " full length sequence" renders claim 3 indefinite.

C) Claim 3 is indefinite because it cannot be determined as to whether the set of probes refers to the probes binding to each of the listed SEQ ID NOs, or any part or combination of the SEQ ID NOs or to a mixture of more than one probe that bind to any one SEQ ID Nos.

D) The term "highlighted regions" render claims 7-16 because it cannot be determined to which or what regions are being referred to. Moreover, SEQ ID NO:1 does not have highlighted positions when referring to Figure 1.

E) Claims 11-16 are indefinite. It cannot be determined as to how probe hybridize to a segment a SEQ ID NO:1 and not hybridize to M. tuberculosis sequence of SEQ ID NO:1. Moreover, as hybridization depends on the hybridization conditions i.e. salt, temperature etc., It is unclear as to what properties the probe possess to satisfy the functional limitation.

F) Claims 6 & 10 are confusing because it cannot be determined whether the ten sequences encompass each and every SEQ ID Nos 1-10 or ten parts from any one or more of the SEQ ID Nos 1-10.

G) The language of "corresponding position" renders claims 7-10 confusing. It cannot be determined whether the method would actually require anymore knowledge than just one of the sequences. When one sequence is compared and matched to a known sequence, each nucleotide at each position is compared and hence each position in the sequence has been examined.

Claim Rejections - 35 USC § 102

9. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

10. Claim 1,7 & 11-16 are rejected under 35 U.S.C. 102(b) as being anticipated by De Beenhouwer et al (WO 95/33851 14 December 1995).

De Beenhouwer et al teach a method of simultaneous detection of the antibiotic resistance and identification mycobacterium species (see whole doc,). They teach that isolating and concentrating polynucleic acids in sample, amplify rpoB gene and hybridize with rpoB probes to differentiate several non-M. tuberculosis isolates (see abstract & claim 1). They teach M. avium 5887 rpoB sequence which contains 72 contiguous base pairs (bp252-324) that are complementary to claimed SEQ ID No. 10 (bp219-291) which contains the highlighted bp 245, 251 & 257. They teach M. avian ITG 5887 rpoB sequence which contains 267 contiguous base

251 & 257. They teach M. avian ITG 5887 rpoB sequence which contains 267 contiguous base pairs (bp 57-324) that are 100% complementary to SEQ. ID NO. 7 (bp 24-291) (see Figure 6 & claim 13) which contains the highlighted base pair 32,33,47,50,53,56,59, 93,94,98,129, 131,146,161,164, 167,176 & 179 . They teach a sequence of M. paratuberculosis strain 316F rpoB which contains 67 contiguous base pairs (bp 252-319) that are 100% complementary to SEQ. ID NO. 8 (bp201-268) (see Figure 6 & claim 13) which contains highlighted base pair 218. They then teach that these non Tuberculosis sequences were sequenced and compared to rpoB gene sequence of M. tuberculosis in order to develop probes which differentiate M. tuberculosis form other species (see page 30-31). Specifically they teach a 22 bp oligonucleotide MA-POL-1 which is perfectly complementary bp 41-63 of SEQ ID NO:7 and contains Figure 1's highlighted base pairs 47,50,53,56 & 59 at its 3'end and central region (see page 40 & Figure 6) and is used to differentiate the strain M. avium (see claim 1, table 2 and page 31 line 1).

11. Claims 1 & 2 are rejected under 35 U.S.C. 102(b) as being anticipated by Miller et al (Antimicrob. Agents Chemother. Vol. 38 (4) pp. 805-811 1994).

Miller et al teach of SacI fragments of M. tuberculosis H37Rv containing the complete rpoB sequence that encodes the beta subunit of RNA polymerase. According to the STIC sequence search SEQ ID NO:1 is 100% complementary.

Claim Rejections - 35 USC § 103

12. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

13. Claim 3 is rejected under 35 U.S.C. 103(a) as being unpatentable over Miller et al (Antimicrob. Agents Chemother. Vol. 38 (4) pp. 805-811 1994).

Miller et al teach of SacI fragments of M. tuberculosis H37Rv containing the complete rpoB sequence that encodes the beta subunit of RNA polymerase. According to the STIC sequence search SEQ ID NO:1 is 100% complementary. They teach several probes thatencompass the rpoB gene particularly they teach of 619 bp probe that spans most of the rpoB gene and 200 bp probes thtat span the 3' end (see figure 1).

Miller et al do not explicitly teach a probe that fully spans the rpoB gene.

One of ordinary skill in the art would have been motivated to design a probe that spans the rpoB gene in order to detect and select rpoB genes from libraries. Miller et al teach the design of probes for the rpoB gene and actually discloses the full sequence of the gene. Moreover, it was well known and practiced in the art at the time of the invention to design primers from known sequences. It would have been prima facie obvious to design a probe from the Miller et al's sequence in order to detect and clone the full sequence gene.

14. Claims 4 & 5 are rejected under 35 U.S.C. 103(a) as being unpatentable over Telenti et al (Lancet vol. 341 pp. 647-650 March 13, 1993) in view of Miller et al (Antimicrob. Agents Chemother. Vol. 38 (4) pp. 805-811 1994).

Telenti et al teach performing a method of detecting and classifying M. tuberculosis by their antibiotic resistance by their sequence. They take DNA from clinical isolates form patients from diverse geographical locations and perform PCR by using primers that amplify a highly

conserved 411 bp region of rpoB gene. They evaluated the isolates for rifampicin sensitive phenotype and compared the rpoB sequences to M. tuberculosis H37v rpoB gene.

Telenti et al do not explicitly teach SEQ ID NO:1.

Miller et al teach of SacI fragments of M. tuberculosis H37Rv containing the complete rpoB sequence that encodes the beta subunit of RNA polymerase. According to the STIC sequence search the sequence is 100% complementary to SEQ ID NO:1.

One of ordinary skill in the art would have motivated to apply Miller et al's disclosed sequence of M. tuberculosis H37Rv in Telenti et al's classification method in order correlate the rifampicin phenotype with the sequence mutations of the sample isolates. Miller et al discloses that their sequence was from a virulent rifampin susceptible strain. It would have been prima facie obvious to apply Miller et al's specific H37Rv sequence which was known to be rifampicin sensitive as a control to compare Telenti et al's sequences in order to correlate mutations in the isolates to rifampicin resistance or sensitivity.

15. Claims 8-10 are rejected under 35 U.S.C. 103(a) as being unpatentable over De Beenhouwer et al (WO 95/33851 14 December 1995).

De Beenhouwer et al teach a method of simultaneous detection of the antibiotic resistance and identification mycobacterium species (see whole doc,). They teach that isolating and concentrating polynucleic acids in sample, amplify rpoB gene and hybridize with rpoB probes to differentiate several non-M. tuberculosis isolates (see abstract & claim 1). They teach M. avium 5887 rpoB sequence which contains 72 contiguous base pairs (bp252-324) that are

complementary to claimed SEQ ID No. 10 (bp219-291) which contains the highlighted positions bp 245, 251 & 257. They teach M. avian ITG 5887 rpoB sequence which contains 267 contiguous base pairs (bp 57-324) that are 100% complementary to SEQ. ID NO. 7 (bp 24-291) (see Figure 6 & claim 13) which contains the highlighted base pair positions 32,33,47,50,53,56,59,93,94,98,129,131,146,161,164,167,176 & 179 . They teach a sequence of M. paratuberculosis strain 316F rpoB which contains 67 contiguous base pairs (bp 252-319) that are 100% complementary to SEQ. ID NO. 8 (bp201-268) (see Figure 6 & claim 13) which contains highlighted position bp 218. They then teach that these non Tuberculosis sequences were sequenced and compared to with rpoB gene sequence of M. tuberculosis in order to develop probes which differentiate M. tuberculosis form other species (see page 30-31). Specifically they teach a 22 bp probe MA-POL-1 which is perfectly complementary bp 41-63 of SEQ ID NO:7 and contains Figure 1's highlighted base pairs 47,50,53,56 & 59 at its 3'end and central region (see page 40 & Figure 6) and is used to differentiate the strain M. avium (see claim 1, table 2 and page 31 line 1).

De Beenhouwer et al do not explicitly teach the identification of at least 10 highlighted bases in Figure 1 in determining species characterization.

One of ordinary skill in the art would have been motivated to apply De Beenhouwer et al's teaching M. avium ITG 5887 rpoB contains sequence in order identify M. avium strain. De Beenhouwer strongly suggests that using the sequence is useful in designing probes to differentiate strains and detect antibiotic resistance (see page 30 lines 10-12 & pg. 31 line 7). It would have been prima facie obvious to use De Beenhouwer et al's disclosed M. avium ITG 5887 rpoB sequence to not only design probes that would contain the highlighted regions but

also provide comparison with other sequences from isolates in order to positively identify the M. avium strain.

SUMMARY

1. There is no prior art that teach or suggest the method of classifying involving comparing with every SEQ ID NO: 1 to 10. In so far as the method claim 6 were to read on comparing with at least each and every SEQ ID 1 to10, claim 6 would be allowable if rewritten to overcome the rejection(s) under 35 U.S.C. 112, second paragraph, set forth in this Office action and to include all of the limitations of the base claim and any intervening claims.

While there is much prior art on the M. tuberculosis rpoB sequence and mutations that correlate with rifampicin resistance and DeBeenhauwer teach many different Mycobacterium strains sequences that contain portions that are 100% complementary to part of the claimed SEQ Ids 2-10, there is no prior art that teach or suggest SEQ ID NOs 2 through 10.

Gingeras et al Genome Research Vol. 8 (5) pp. 435-448 1998 is enclosed as a reference showing the state of art. The STIC sequence matches with SEQ ID 1,7,8 & 10 are enclosed.

CONCLUSION

2. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Jeffrey Siew whose telephone number is (703) 305-3886 and whose e-mail address is Jeffrey.Siew@uspto.gov. The examiner can best be reached on Monday

through Thursday from 6:30 a.m. to 4 p.m. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Margaret Parr, can be reached on (703) 308-2454.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist for Technology Center 1600 whose telephone number is (703) 308-0196.

Papers related to this application may be submitted to Group 1600 by facsimile transmission. Papers should be faxed to Group 1600 via the PTO Fax Center located in Crystal Mall 1. The faxing of such papers must conform with the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989). The CM1 Center numbers for Group 1600 are Voice (703) 308-3290 and Fax (703) 308-4556 or (703) 308-4242.

JS

Jeffrey Siew

January 27, 2001

RESULT 2
MSGRPOB
LOCUS MSGRPOB 5084 bp DNA BCT 13-SEP-1994
DEFINITION Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene, complete cds and RNA polymerase beta'-subunit rpoC gene, partial cds.
ACCESSION L27989
VERSION L27989.1 GI:468333
KEYWORDS RNA polymerase beta-subunit; rpoB gene.
SOURCE Mycobacterium tuberculosis (strain Rv) DNA.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 5084)
AUTHORS Miller,L.P., Crawford,J.T. and Shinnick,T.M.
TITLE The rpoB gene of Mycobacterium tuberculosis
JOURNAL Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
MEDLINE 94304130
FEATURES Location/Qualifiers
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ORIGIN


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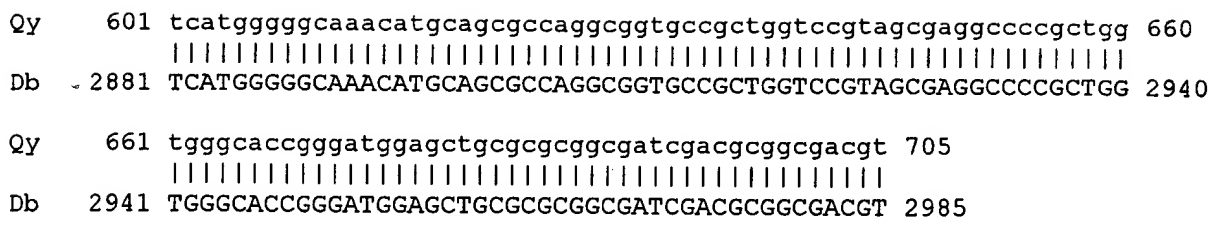
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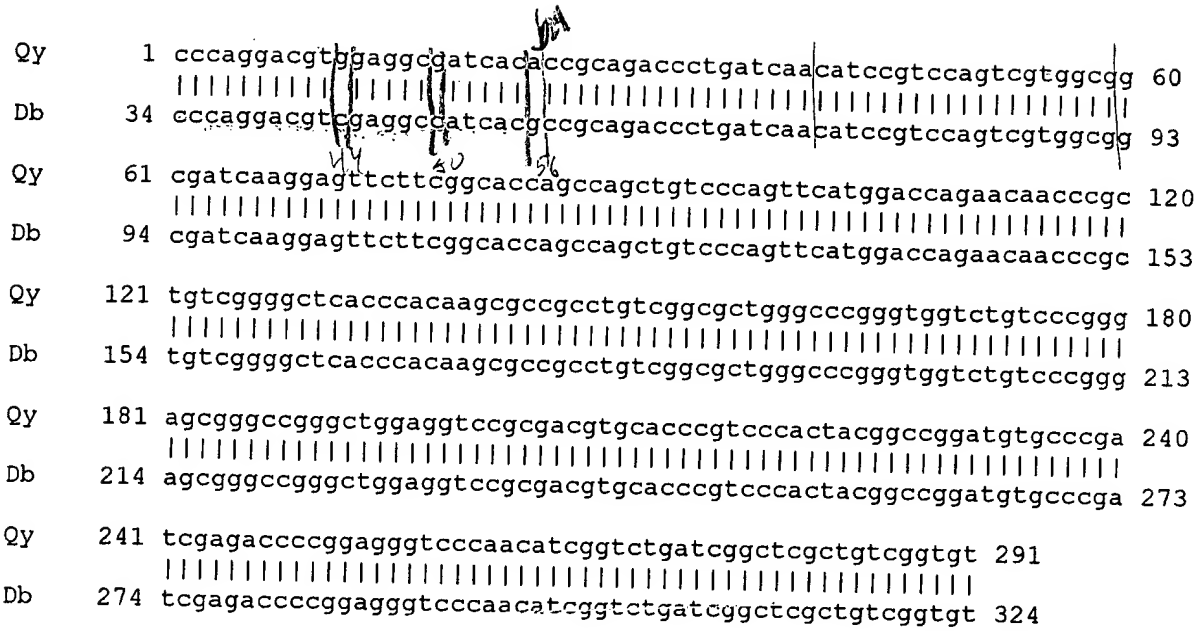
RESULT 7
T29614
ID T29614 standard; DNA; 324 BP.
XX
AC T29614;
XX
DT 10-JUL-1996 (first entry)
XX
DE Partial sequence of M. avium strain ITG 5887 rpoB gene.
XX
KW Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; avium; rpoB; fragment;
KW probe; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Mycobacterium avium.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinckx L, Portaels F;
PI Rossau R;
XX
DR WPI; 1996-040250/04.
XX
PT Probes and primers for determn. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 13; Fig 6; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, hybridising it with at least 1 rpoB gene probe,
CC detecting the hybrids formed and inferring the ARS, and opt. the
CC spp. using species specific probes (i.e. T12145 derived from the
CC present sequence, the partial nucleotide sequence of the
CC presumptive M. avium strain ITG 5887 rpoB gene) from the
CC differential hybridisation patterns. The method is partic. useful
CC for the detection of rifampicin and/or rifabutin resistance in
CC M. leprae or M. tuberculosis, and mycobacterial spp.
CC identification. The method is rapid and reliable and provides
CC simultaneous determn. of ARS and spp. identity.
XX
SQ Sequence 324 BP; 52 A; 114 C; 108 G; 50 T; 0 other;

Query Match 40.6%; Score 286.2; DB 17; Length 324;
Best Local Similarity 99.0%; Pred. No. 3.6e-42;
Matches 288; Conservative 0; Mismatches 3; Indels 0; Gaps 0;


Qy 1 cccaggacgtcgaggccatcacaccgcagaccctgatcaacatccgtccagtcgtggcgg 60
Db 34 cccaggacgtcgaggccatcacgccgcagaccctgatcaacatccgtccagtcgtggcgg 93
Qy 61 cgatcaaggagttcttcggcaccagccagctgtcccagttcatggaccagaacaacccgc 120
Db 94 cgatcaaggagttcttcggcaccagccagctgtcccagttcatggaccagaacaacccgc 153
Qy 121 tgtcggggctcacccacaagcgccgcctgtcggcgctgggcccgggtggtctgtcccggg 180
Db 154 tgtcggggctcacccacaagcgccgcctgtcggcgctgggcccgggtggtctgtcccggg 213
Qy 181 agcgggccgggctggaggtccgcgacgtgcacccgtcccactacggccggatgtgcccga 240
Db 214 agcgggccgggctggaggtccgcgacgtgcacccgtcccactacggccggatgtgcccga 273
Qy 241 tcgagaccccggagggtcccaacatcggtctgatcggctcgctgtcggtgt 291
Db 274 tcgagaccccggagggtcccaacatcggtctgatcggctcgctgtcggtgt 324

RESULT 8
T29613
ID T29613 standard; DNA; 319 BP.
XX
AC T29613;
XX
DT 10-JUL-1996 (first entry)
XX
DE Partial sequence of M. paratuberculosis strain 316F rpoB gene.
XX
KW Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; paratuberculosis; rpoB; fragment;
KW probe; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Mycobacterium paratuberculosis.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinckx L, Portaels F;
PI Rossau R;
XX
DR WPI; 1996-040250/04.
XX
PT Probes and primers for determn. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 13; Fig 5; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, hybridising it with at least 1 rpoB gene probe,
CC detecting the hybrids formed and inferring the ARS, and opt. the
CC spp. using species specific probes (i.e. T12144 derived from the
CC present sequence, the partial nucleotide sequence of the
CC presumptive M. paratuberculosis strain 316F rpoB gene) from the
CC differential hybridisation patterns. The method is partic. useful
CC for the detection of rifampicin and/or rifabutin resistance in
CC M. leprae or M. tuberculosis, and mycobacterial spp.
CC identification. The method is rapid and reliable and provides
CC simultaneous determn. of ARS and spp. identity.
XX
SQ Sequence 319 BP; 51 A; 105 C; 107 G; 49 T; 7 other;

Query Match 36.3%; Score 255.6; DB 17; Length 319;
Best Local Similarity 96.6%; Pred. No. 7.6e-37;
Matches 258; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db      53 ccaggacgtngaggccatcacgccgcagaccctgatcaacatccgtcccgtcgtggcggc 112

Qy      62 gatcaaggagttcttcggcaccagccagctgtcccagttcatggaccagaacaacccgct 121
           |||||||||||||||||| ||||||||| ||||||||||||||||||||||||||||||
Db     113 gatcaaggagttcttcggnaccagccagttgtcccagttcatggaccagaacaacccgct 172

Qy     122 gtcggggctcacccacaagcgccgcctgtcggcgctgggcccgggtggtctgtcccggga 181
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     173 gtcggggctcacccacaagcgccgcctgtcggcgntgggcccgggtggtctgtcccggga 232

Qy     182 gcgggccgggctggaggtccgcgacgtgcacccgtcccactacggccggatgtgcccgat 241
           |||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||
Db     233 gcgggccgggctggaggtccgngacgtgnacccgtcccactacggccggatgtgcccgat 292

Qy     242 cgagaccccggagggtcccaacatcgg 268
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Db     293 cgagaccccggagggtcccaacatcgg 319
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RESULT 7
T29614
ID T29614 standard; DNA; 324 BP.
XX
AC T29614;
XX
DT 10-JUL-1996 (first entry)
XX
DE Partial sequence of M. avium strain ITG 5887 rpoB gene.
XX
KW Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; avium; rpoB; fragment;
KW probe; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Mycobacterium avium.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinckx L, Portaels F;
PI Rossau R;
XX
DR WPI; 1996-040250/04.
XX
PT Probes and primers for determn. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 13; Fig 6; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, hybridising it with at least 1 rpoB gene probe,
CC detecting the hybrids formed and inferring the ARS, and opt. the
CC spp. using species specific probes (i.e. T12145 derived from the
CC present sequence, the partial nucleotide sequence of the
CC presumptive M. avium strain ITG 5887 rpoB gene) from the
CC differential hybridisation patterns. The method is partic. useful
CC for the detection of rifampicin and/or rifabutin resistance in
CC M. leprae or M. tuberculosis, and mycobacterial spp.
CC identification. The method is rapid and reliable and provides
CC simultaneous determn. of ARS and spp. identity.
XX
SQ Sequence 324 BP; 52 A; 114 C; 108 G; 50 T; 0 other;

Query Match 39.6%; Score 279; DB 17; Length 324;
Best Local Similarity 96.9%; Pred. No. 6.4e-41;
Matches 282; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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Db      34 cccaggacgtcgaggccatcacgccgcagaccctgatcaacatccgtccagtcgtggcgg 93

Qy      61 cgatcaaggagttcttcggcaccagccagctgtcccagttcatggaccagaacaacccgc 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      94 cgatcaaggagttcttcggcaccagccagctgtcccagttcatggaccagaacaacccgc 153

Qy     121 tgtcgggtctgacccacaagcgccgcctgtcggcgctgggcccgggtggtctgtcccggg 180
           ||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     154 tgtcggggctcacccacaagcgccgcctgtcggcgctgggcccgggtggtctgtcccggg 213

Qy     181 agcgggccggcctggaggtccgtgacgtgcacccgtcscactacggccggatgtgcccga 240
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Qy     241 tcgagaccccggagggtcccaacatcggtctgatcggctcgctgtcggtgt 291
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